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Antigenic diversity and evolution of swine influenza viruses: an update

OFFLU swine influenza virus group, Rome 2013

Department of Zoology

UNIVERSITY OF CAMBRIDGE

Initial OFFLU SIV antigenic cartography aim -> 'global' antigenic map of H1 in swine

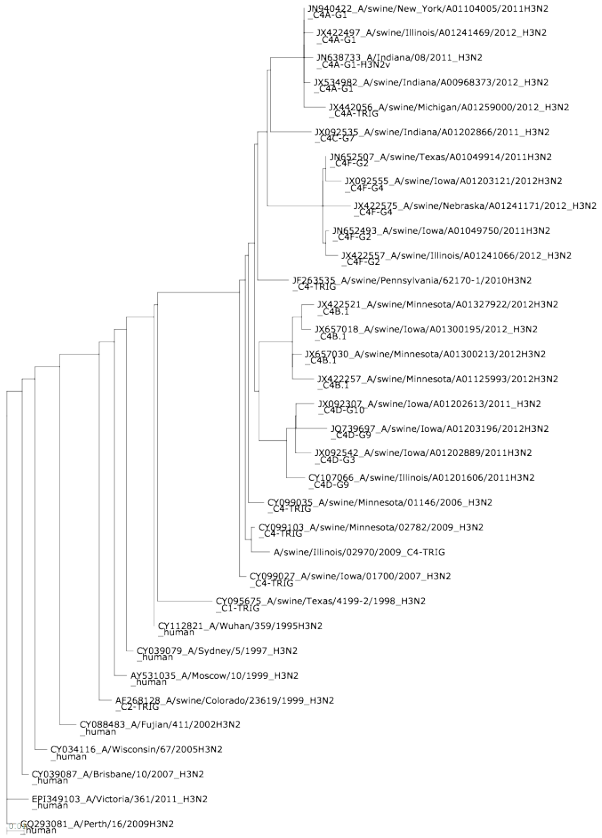
- Characterise the antigenic diversity and evolution of H1 viruses
dataset = 1930-2012, viruses from USA, Canada, EU, Hong Kong,
- genetic evolution - 'global'
- molecular basis for antigenic differences
- rates of antigenic evolution → H1 and H3 ↓

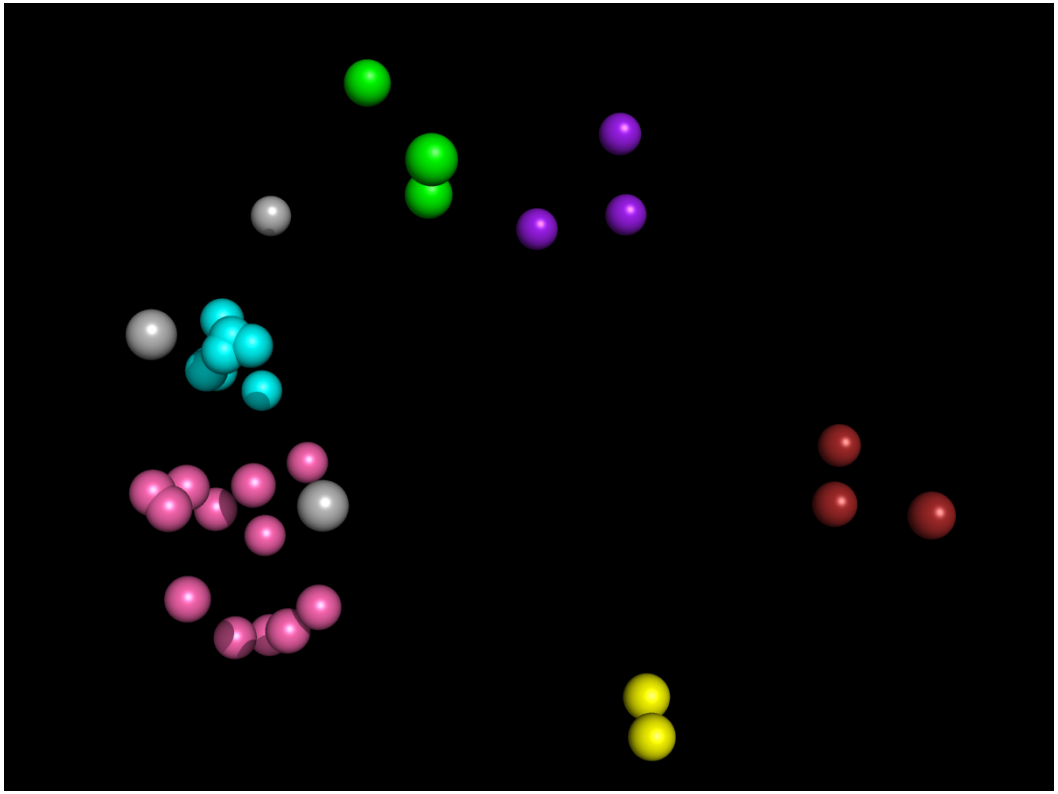
Providing up to date 'global' characterisation of antigenic diversity
Examining relationship where relevant to human flu strains.

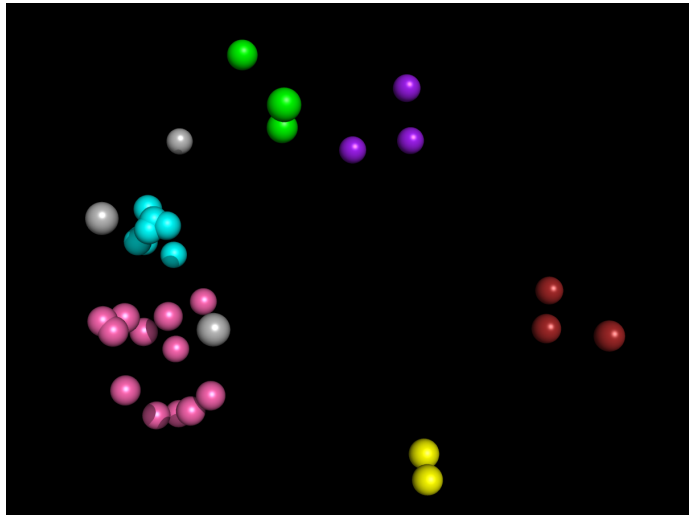
Within-host antigenic evolution: Where are we now?

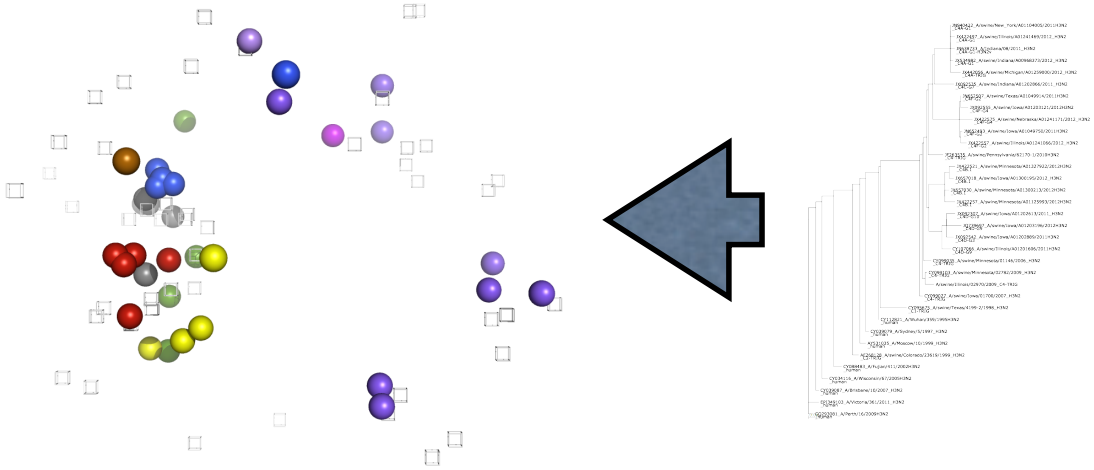
2006-2012

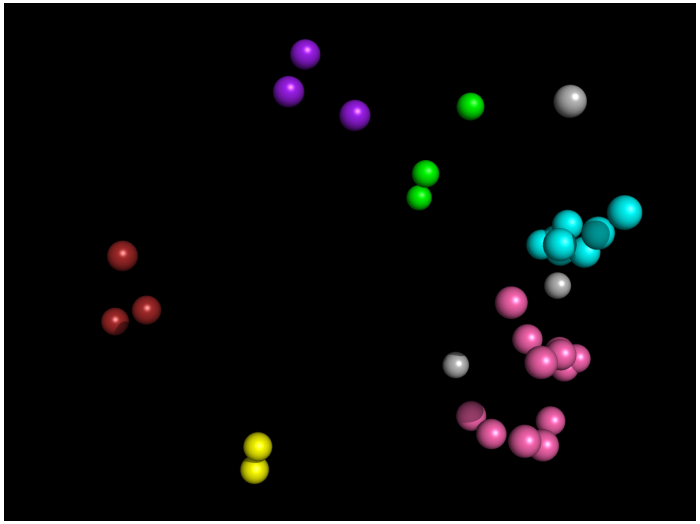
Swine influenza (H3N2) viruses
North America

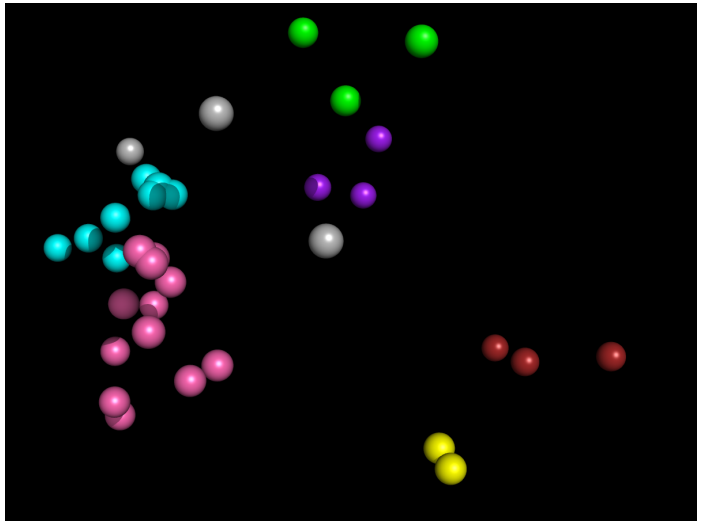






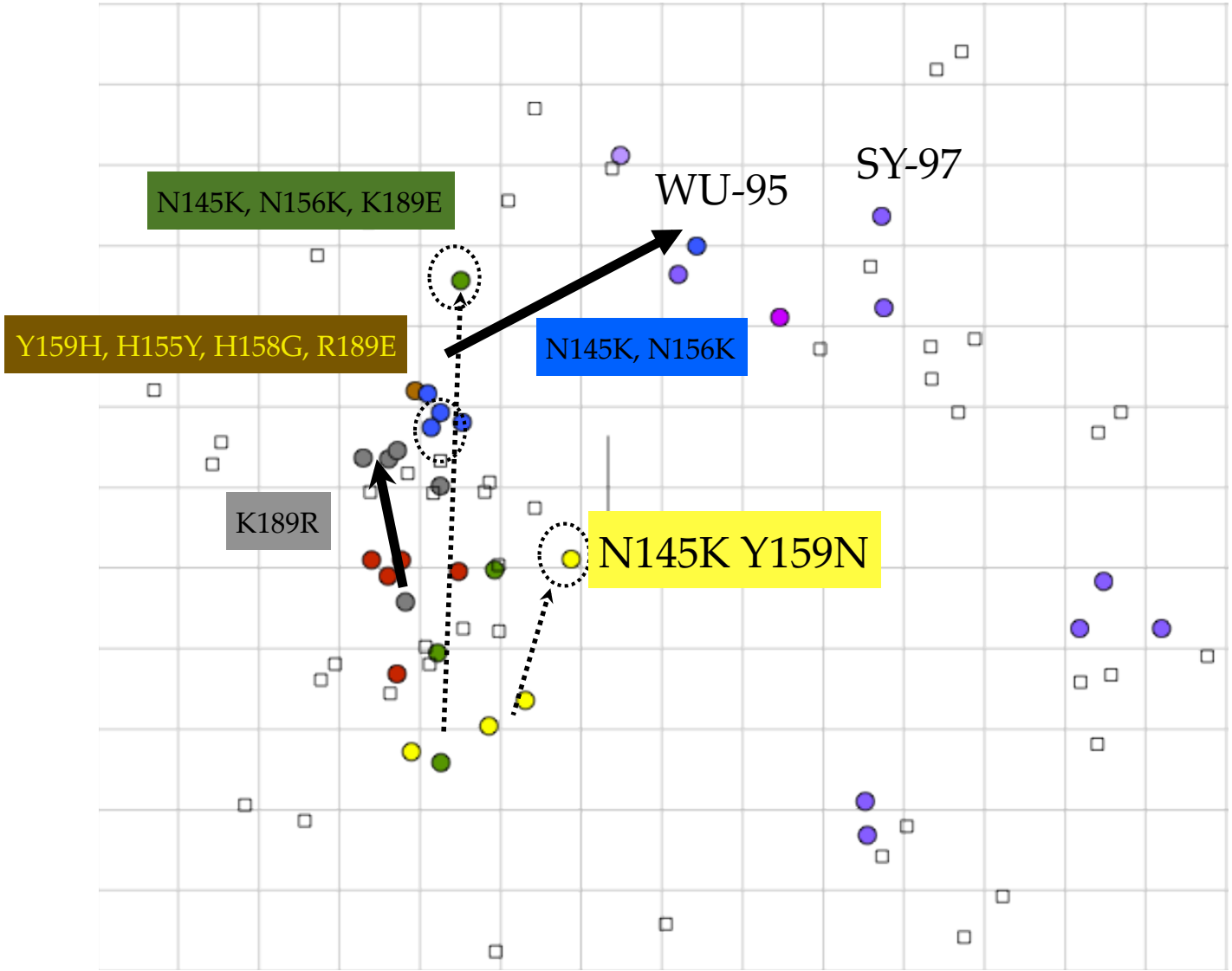






SI-87 ····N145K····▸ Be-89

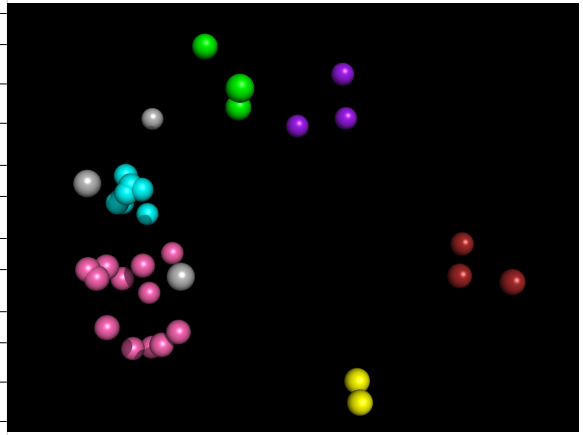
BE-92 ····▸ WU-95

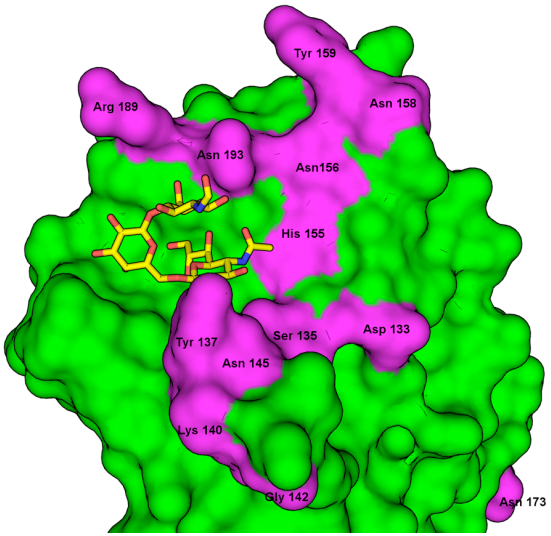


NE/2012 dropped to Vacc 1,2,3

swine=ferret

Genetic clade	Antigenic Cluster	145	155	156	158	159	189
AF268128_A/swine/Colorado/23619/		K	H	**Q**	K	Y	S
AY531035_A/Moscow/10/1999_(H3N2)		K	H	**Q**	K	Y	S
CY039079_A/Sydney/5/1997_(H3N2)_		K	H	**Q**	K	Y	S
CY095675_A/swine/Texas/4199-2/19		K	H	K	E	Y	S
CY112821_A/Wuhan/359/1995(H3N2)_		K	H	K	E	Y	S
JX422575_A/swine/Nebraska/A01241		**K**	H	**K**	N	Y	R
JQ739697_A/swine/Iowa/A01203196/		**K**	H	**K**	N	Y	**E**
JX092535_A/swine/Indiana/A012028		N	Y	**H**	**G**	**H**	**E**
JX422557_A/swine/Illinois/A01241		N	H	N	N	Y	R
JX092555_A/swine/Iowa/A01203121/		N	H	N	N	Y	R
JN652493_A/swine/Iowa/A01049750/		N	H	N	N	Y	R
JN652507_A/swine/Texas/A01049914		N	H	N	N	Y	R
CY099035_A/swine/Minnesota/01146		N	H	N	N	Y	R
CY099027_A/swine/Iowa/01700/2007		N	H	N	D	Y	R
A/swine/Illinois/02970/2009_C4-T		N	T	N	D	Y	R
CY099103_A/swine/Minnesota/02782		N	H	S	N	Y	R
JX092307_A/swine/Iowa/A01202613/		N	H	N	N	Y	K
JX092542_A/swine/Iowa/A01202889/		N	H	N	N	Y	K
CY107066_A/swine/Illinois/A01201		N	Y	N	N	Y	K
JX657030_A/swine/Minnesota/A0130		N	Y	N	N	Y	K
JX657018_A/swine/Iowa/A01300195/		N	Y	N	N	Y	K
JX422521_A/swine/Minnesota/A0132		N	Y	N	N	Y	K
JF263535_A/swine/Pennsylvania/62		N	**Y**	N	N	Y	K
JX442056_A/swine/Michigan/A01259		N	Y	N	N	Y	K
JN638733_A/Indiana/08/2011_(H3N2		N	Y	N	N	Y	K
JX422497_A/swine/Illinois/A01241		N	Y	N	N	Y	K
JN940422_A/swine/New_York/A01104		N	Y	N	N	Y	K
JX534982_A/swine/Indiana/A009683		N	Y	N	N	Y	K
JX422257_A/swine/Minnesota/A0112		**K**	Y	N	N	**N**	K





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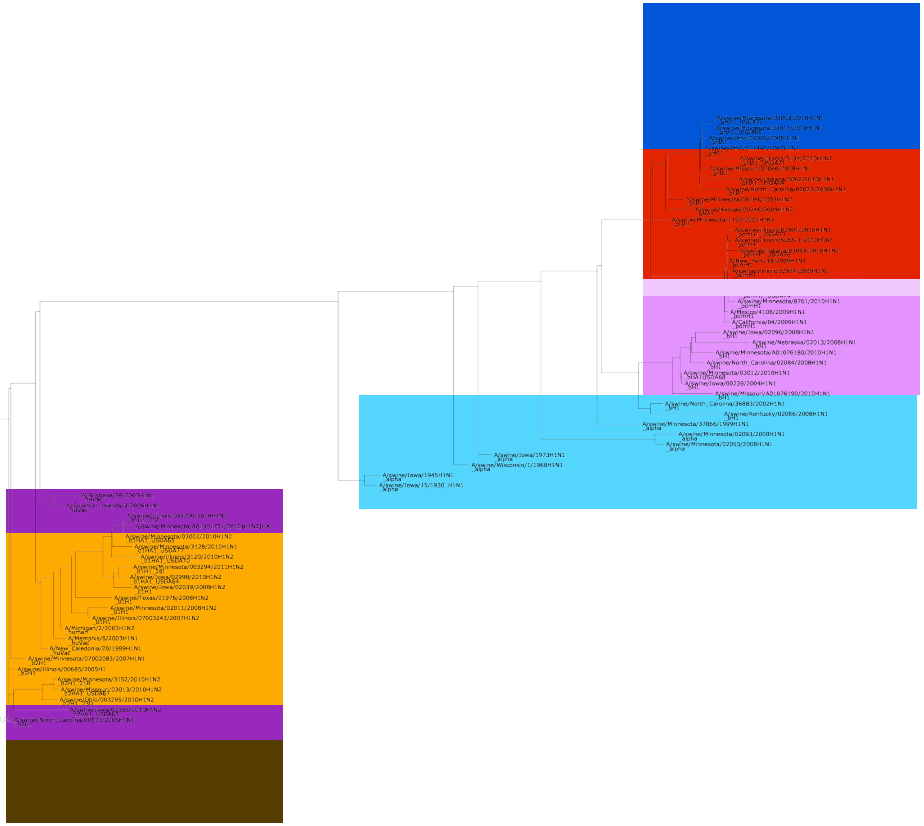
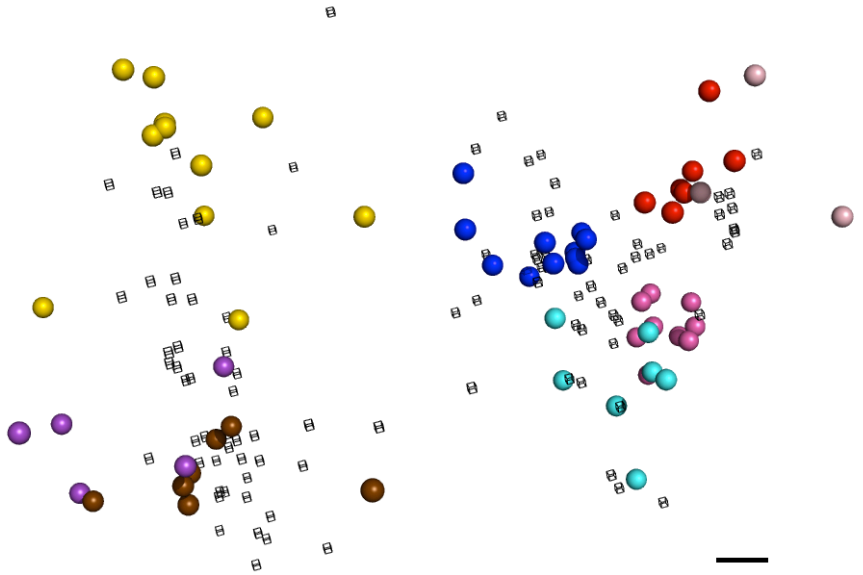
Initial OFFLU SIV antigenic cartography aim -> ‘global’ antigenic map of H1 in swine

- Characterise the antigenic diversity and evolution of H3 swine influenza viruses dataset = United States, EU (ESNIP3.....under way), any other partners?
- genetic evolution - ‘global’ - 2006-2012 phylogenetic tree, significant phylogenetic diversity - not all clades represented antigenically
- molecular basis for antigenic differences -> analyses under way
- rates of antigenic evolution

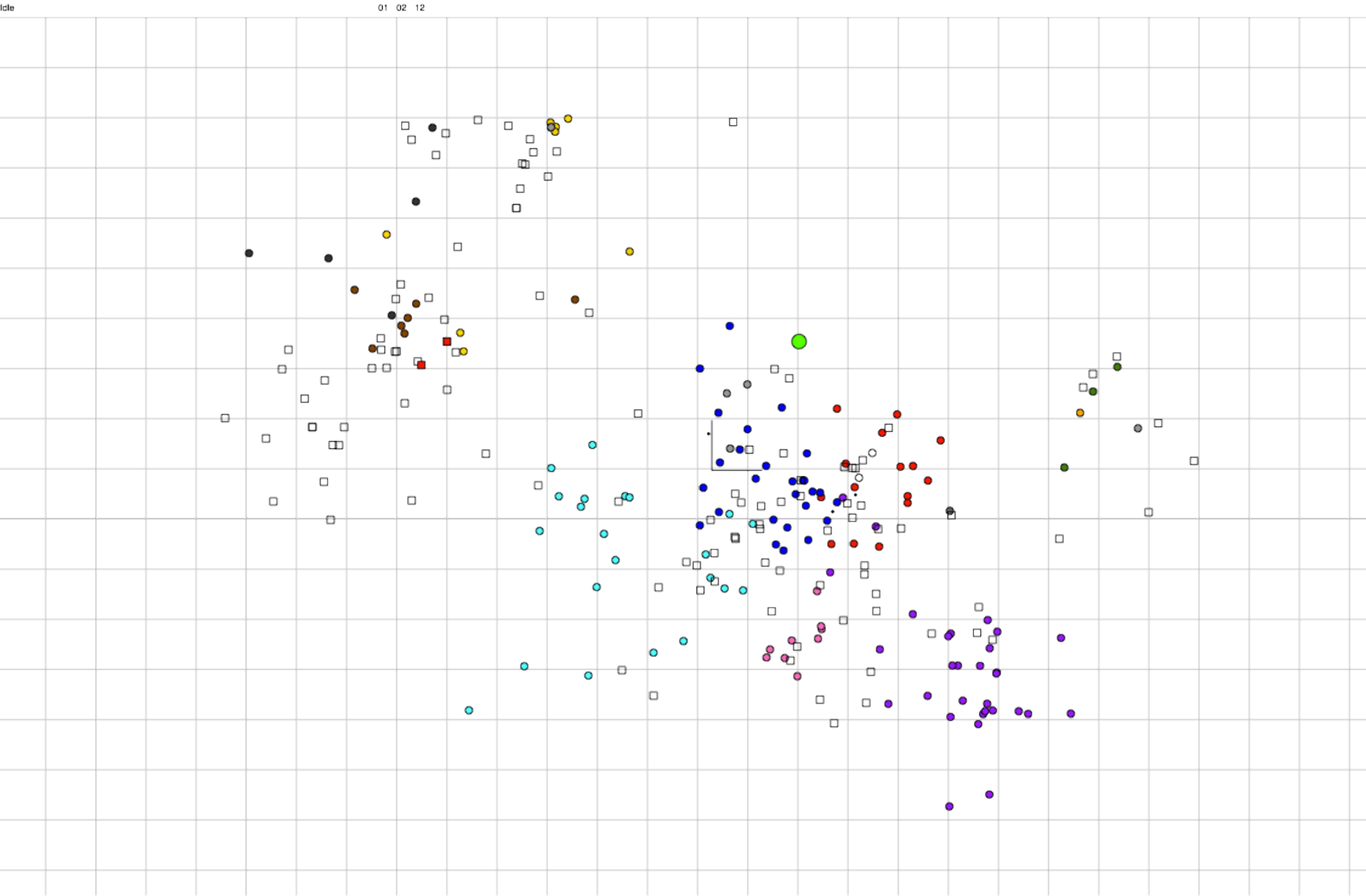
Swine influenza A H1 viruses
North America ->2012

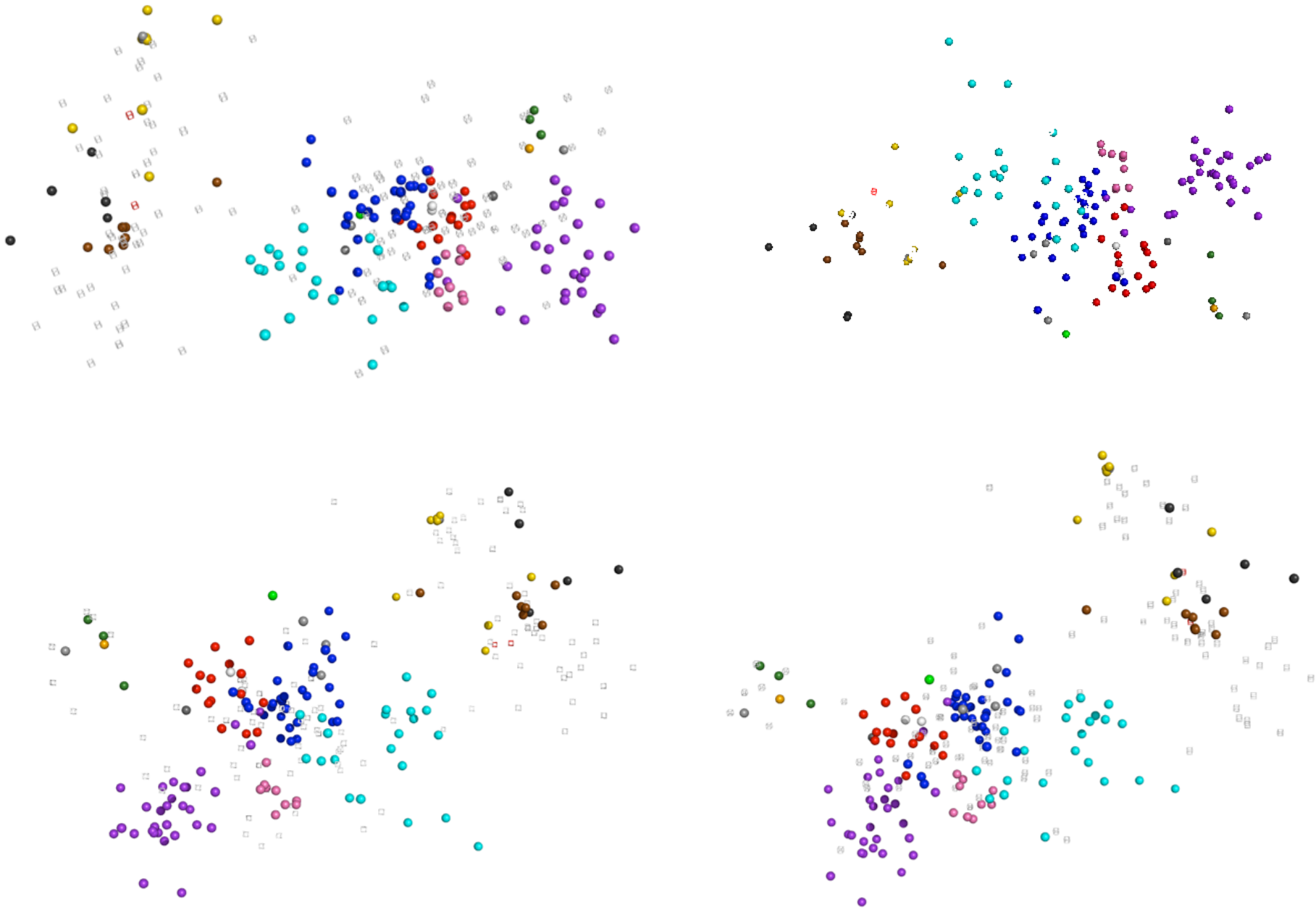




Lorusso,· Vincent, Harland, Alt, Bayles, Swenson, Gramer, Lager, and Lewis

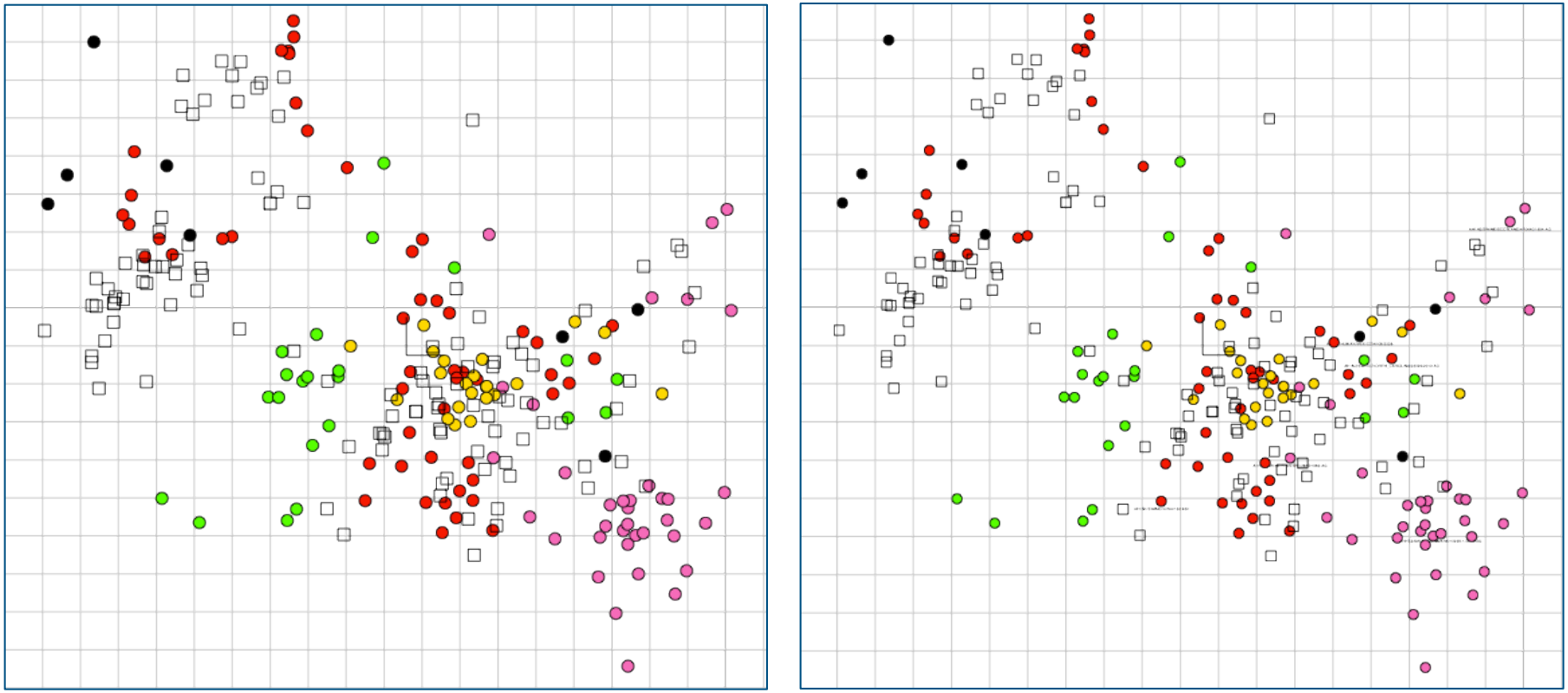
USDA/ARS/NADC, USDA/APHIS/NVSL, University of Minnesota, University of Cambridge. J Gen Virol 92:919-30


Idle
01 02 12

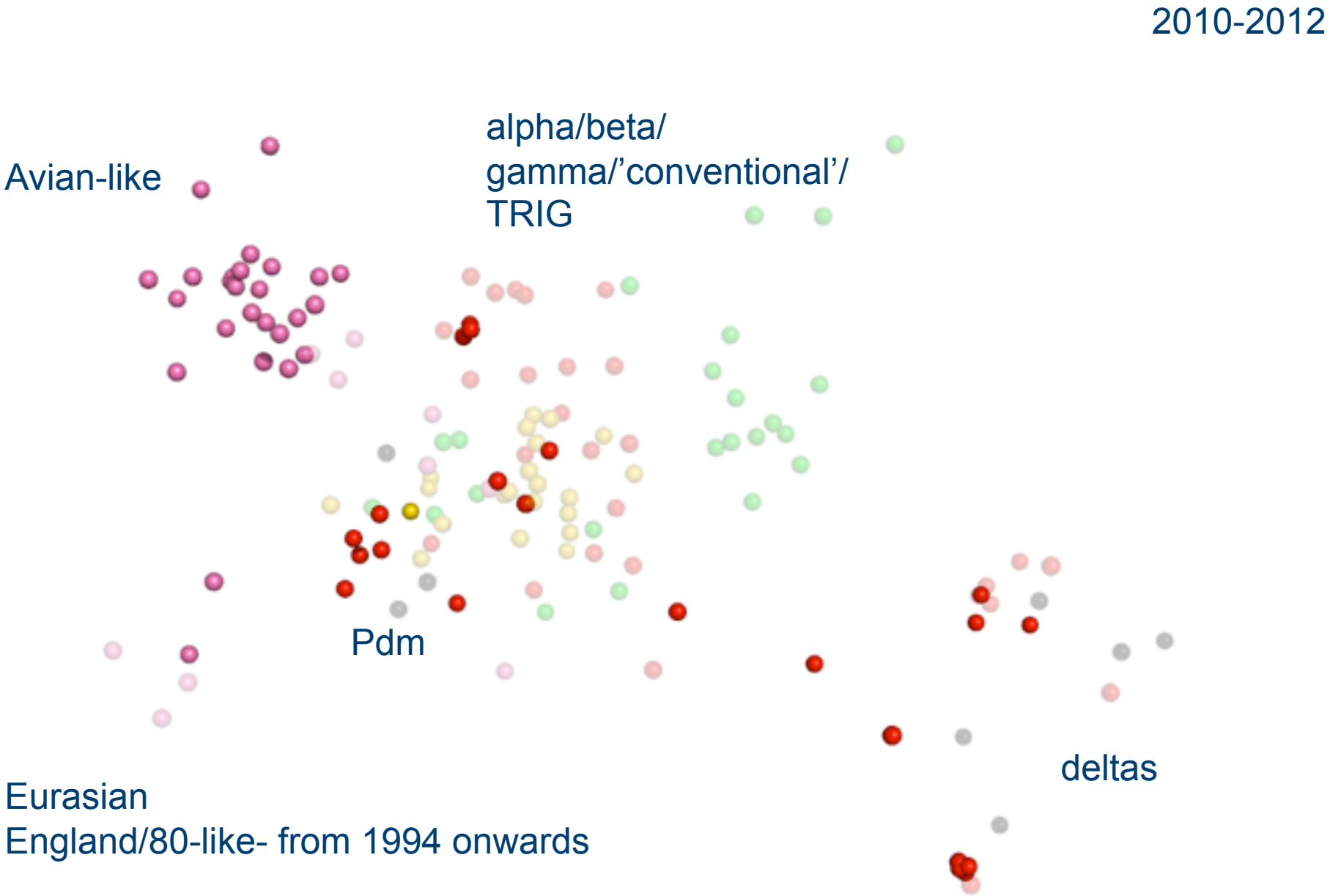


Phylogenetically very diverse

Swine influenza A H1 viruses ‘globally’



Key: Red = USA, Green = Canada, Gold = Hong Kong
Pink = Europe. Black = human viruses


2010-2012
alpha/beta/
gamma/'conventional'/
TRIG
Avian-like
Pdm
deltas
Eurasian
England/80-like- from 1994 onwards

Geographic spatial diversity

2010-2012

The future

- Aim to have ‘globally representative’ antigenic data from all possible geographic regions through 2012 and beyond. Include integration of human flu data where relevant.
- Informing WHO/OIE/FAO with latest: ?through OFFLU or ?WHOCC VCM system for antigenic cartography
  - EU - more Eurasian H1’s ? drift variants, recent avian-like H1’s, HK ? later than 2009?, Add Argentinian data, ? Canadian 26 isolates 2010-2012, other partners with potential antigenic variants
  - H3’s.....EU to be added to USA. Other collaborators
  - *Re-run global SIV phylogenetic trees and finalise genetic basis for differences among clusters.*
  - *Calculate rates of evolution (antigenic and genetic)*
  - *Publication? - OFFLU output for this year*

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ESNIP 3 consortium partners
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ESNIP3:FP7#259949
http://www.esnip3.com/

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